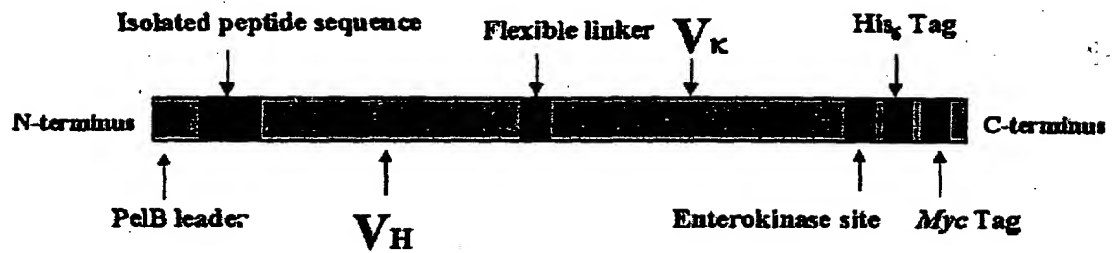
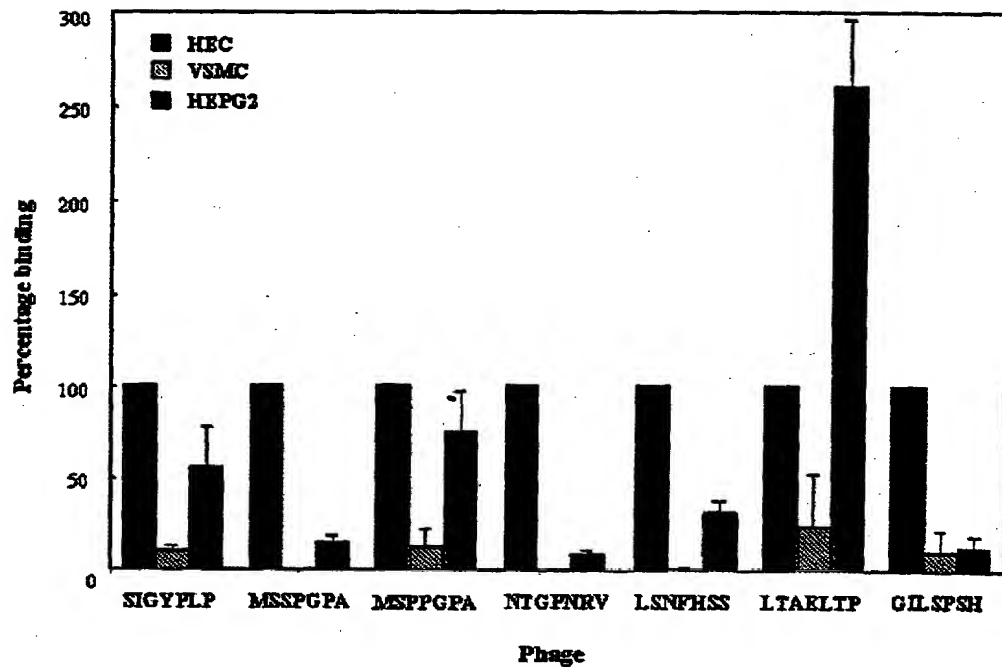
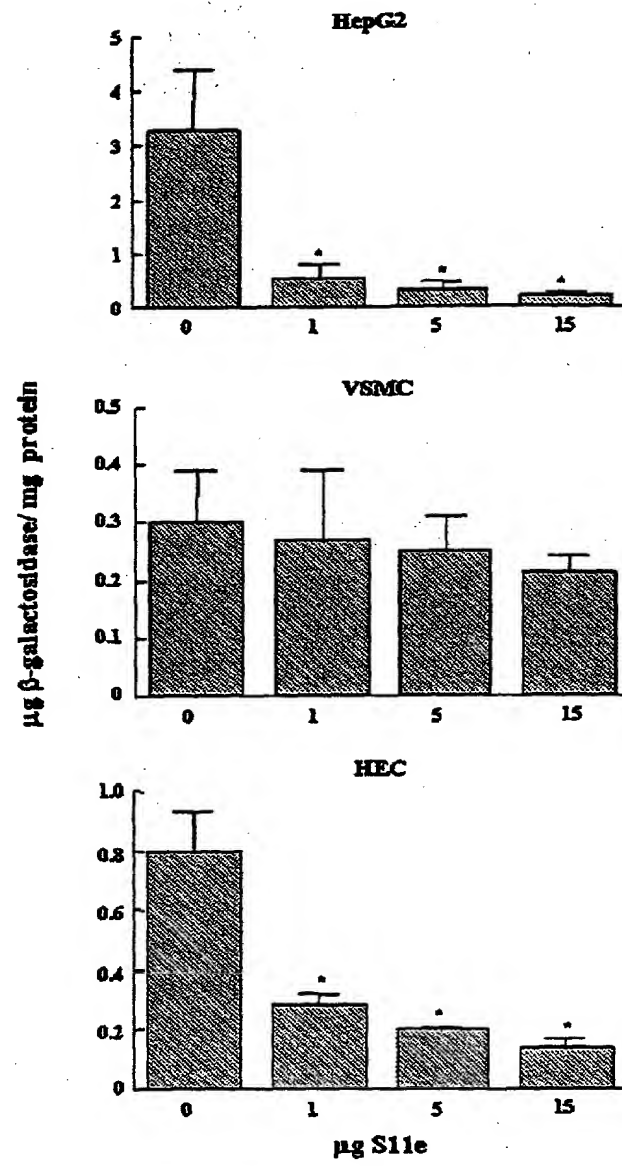
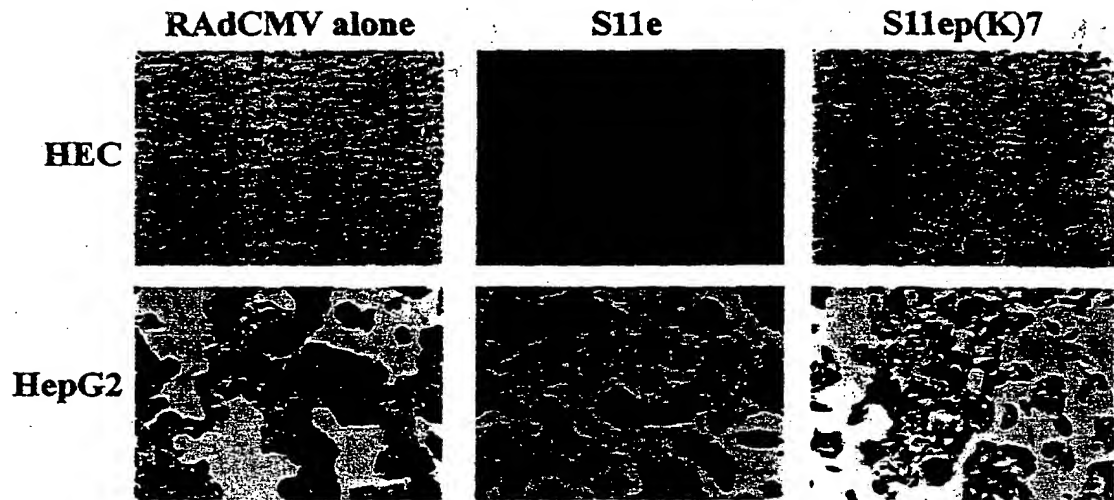
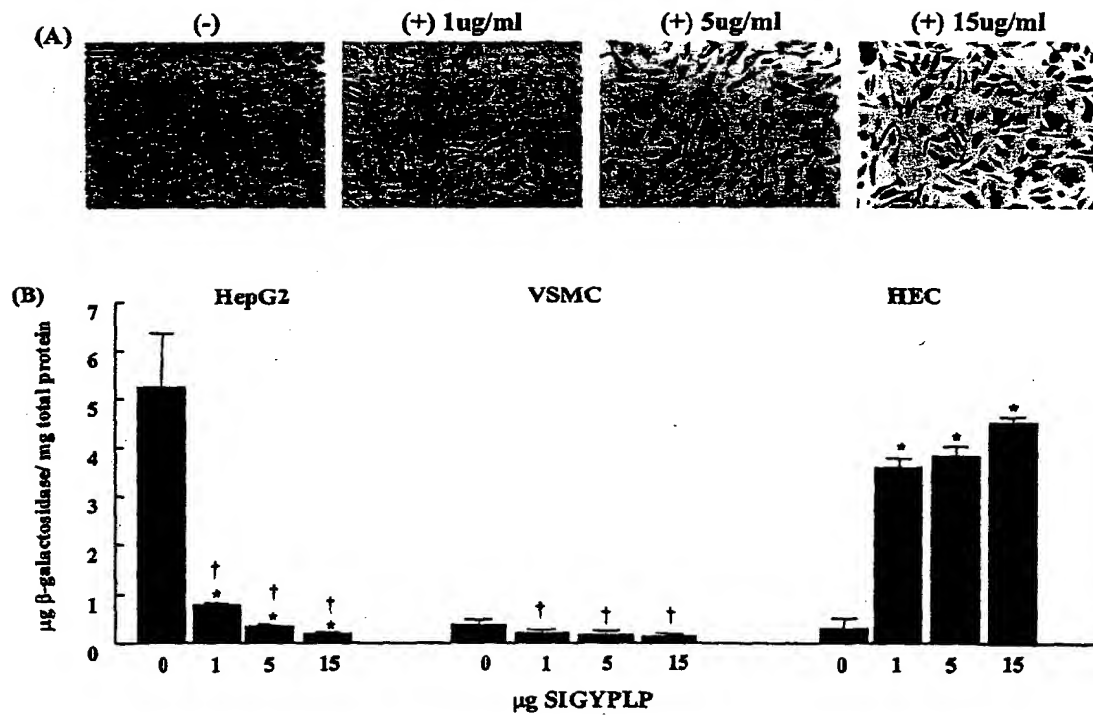
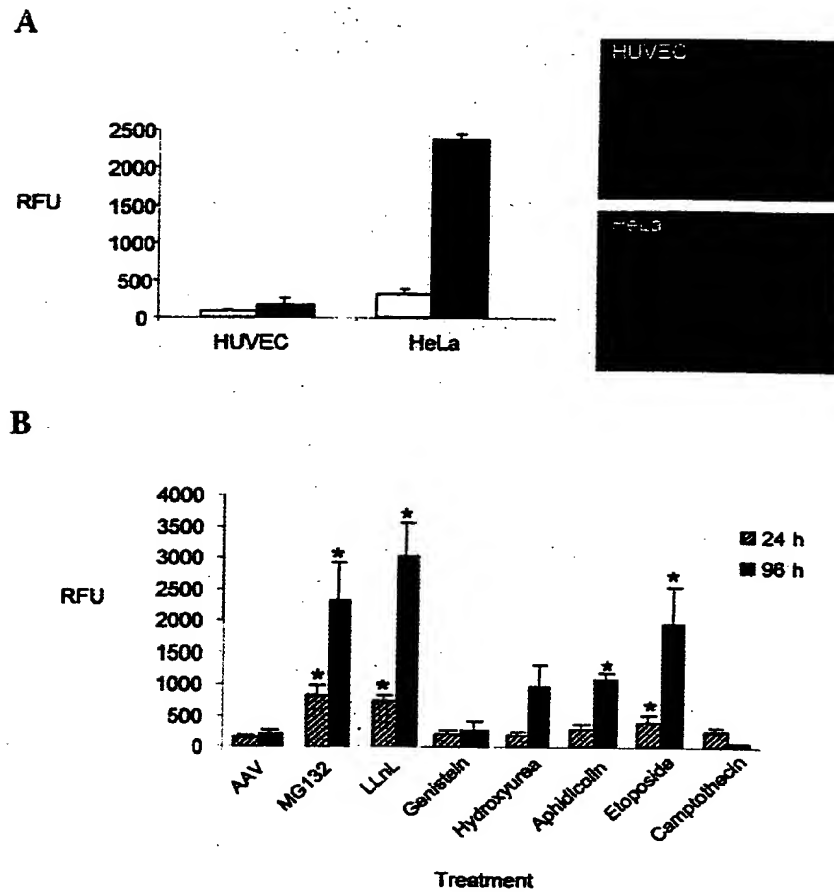
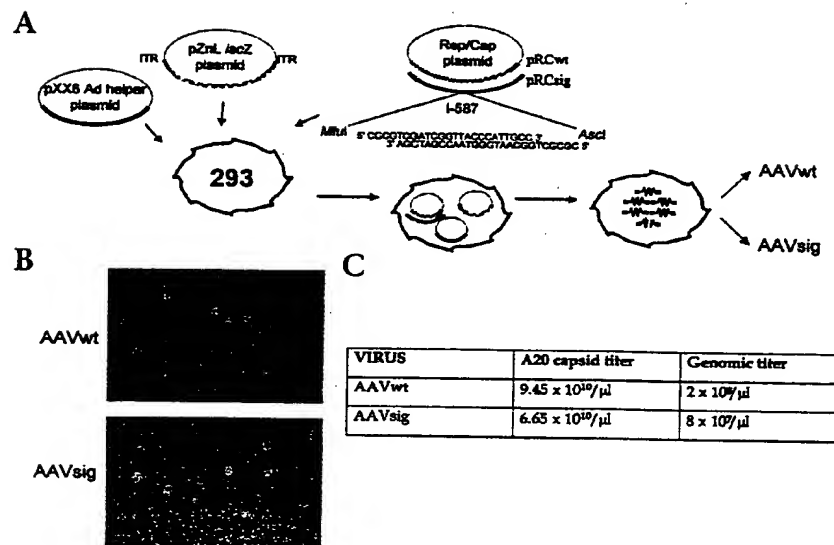
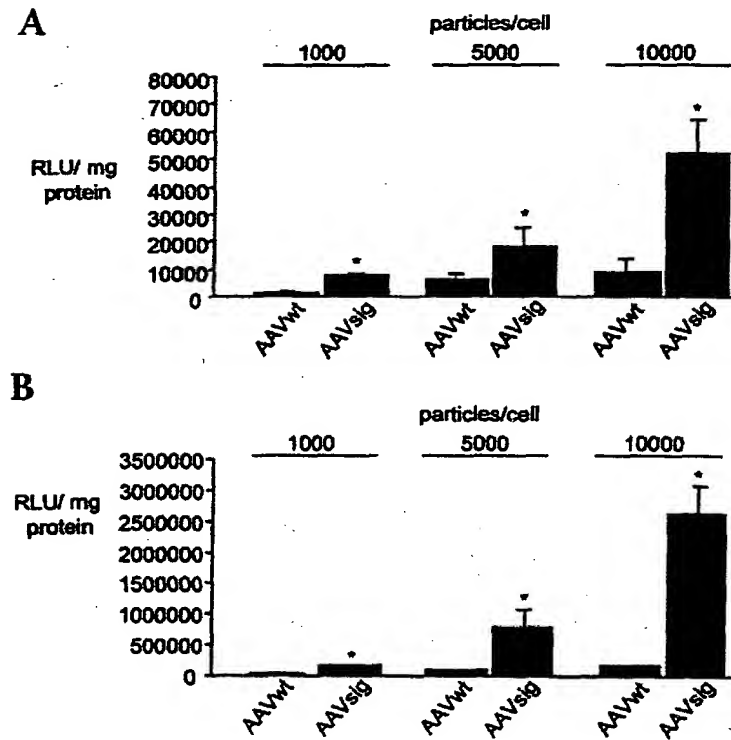
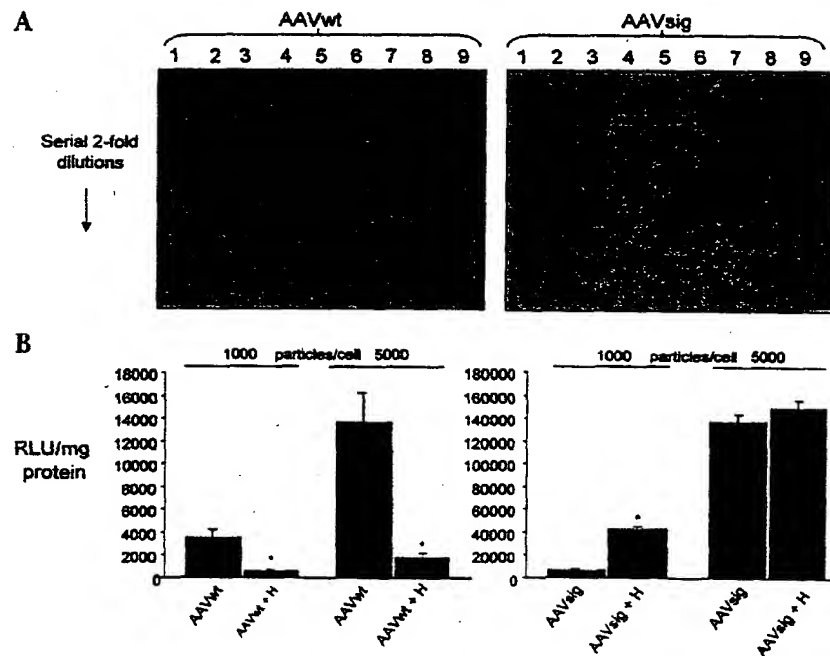


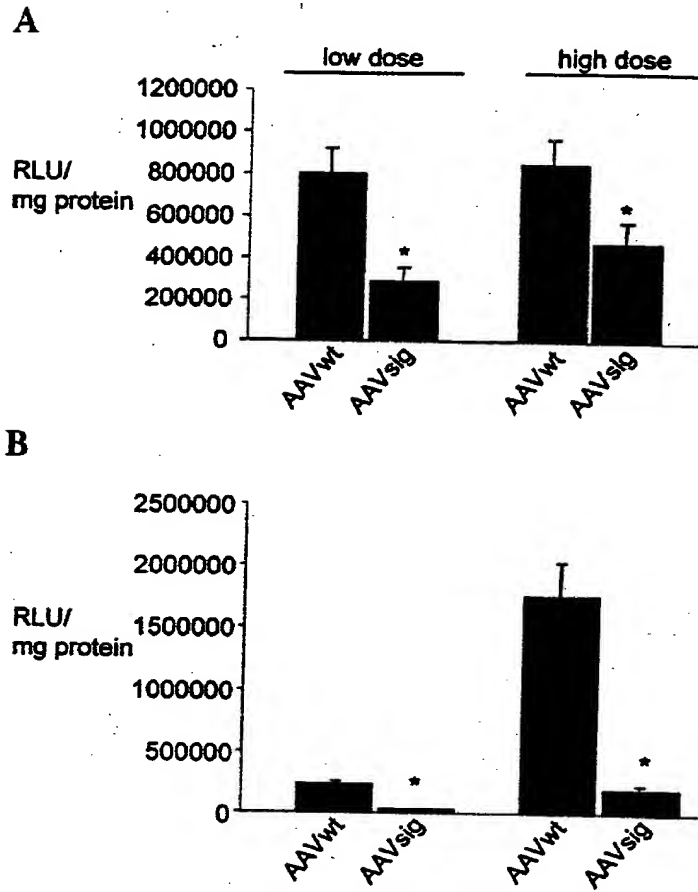
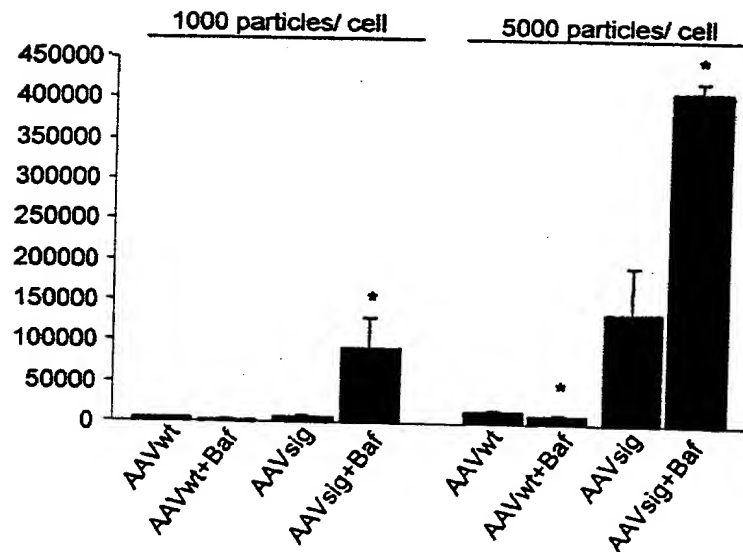
**FIGURE 1****FIGURE 2**

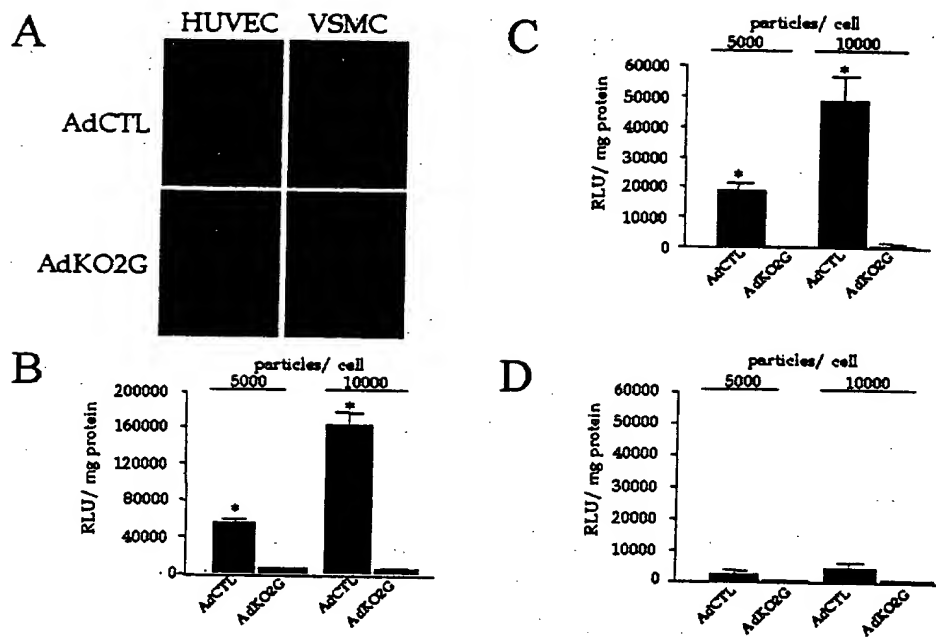
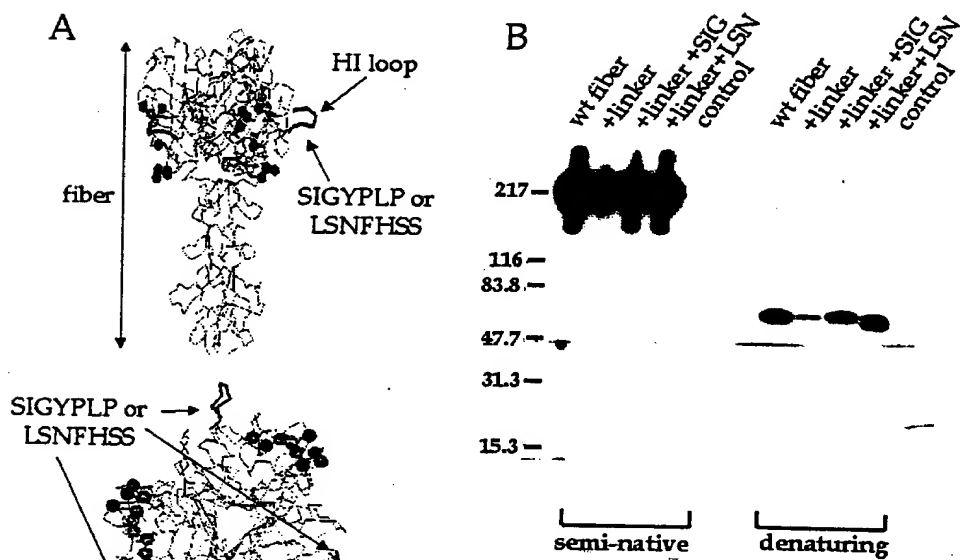
**FIGURE 3**

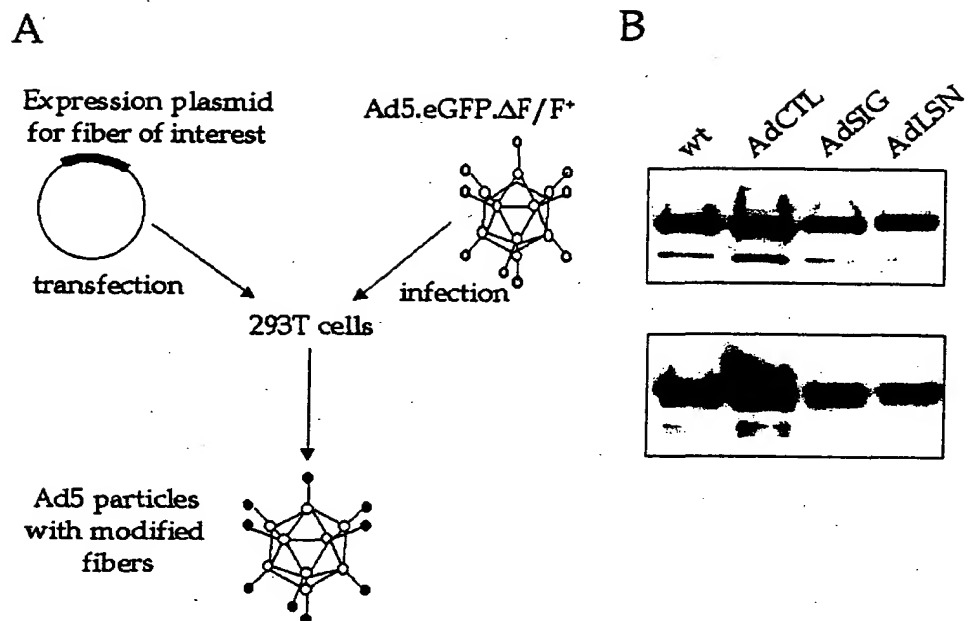
**FIGURE 4****FIGURE 5**

**FIGURE 6****FIGURE 7**

**FIGURE 8****FIGURE 9**

**FIGURE 10****FIGURE 11**

**FIGURE 12****FIGURE 13**

**FIGURE 14**



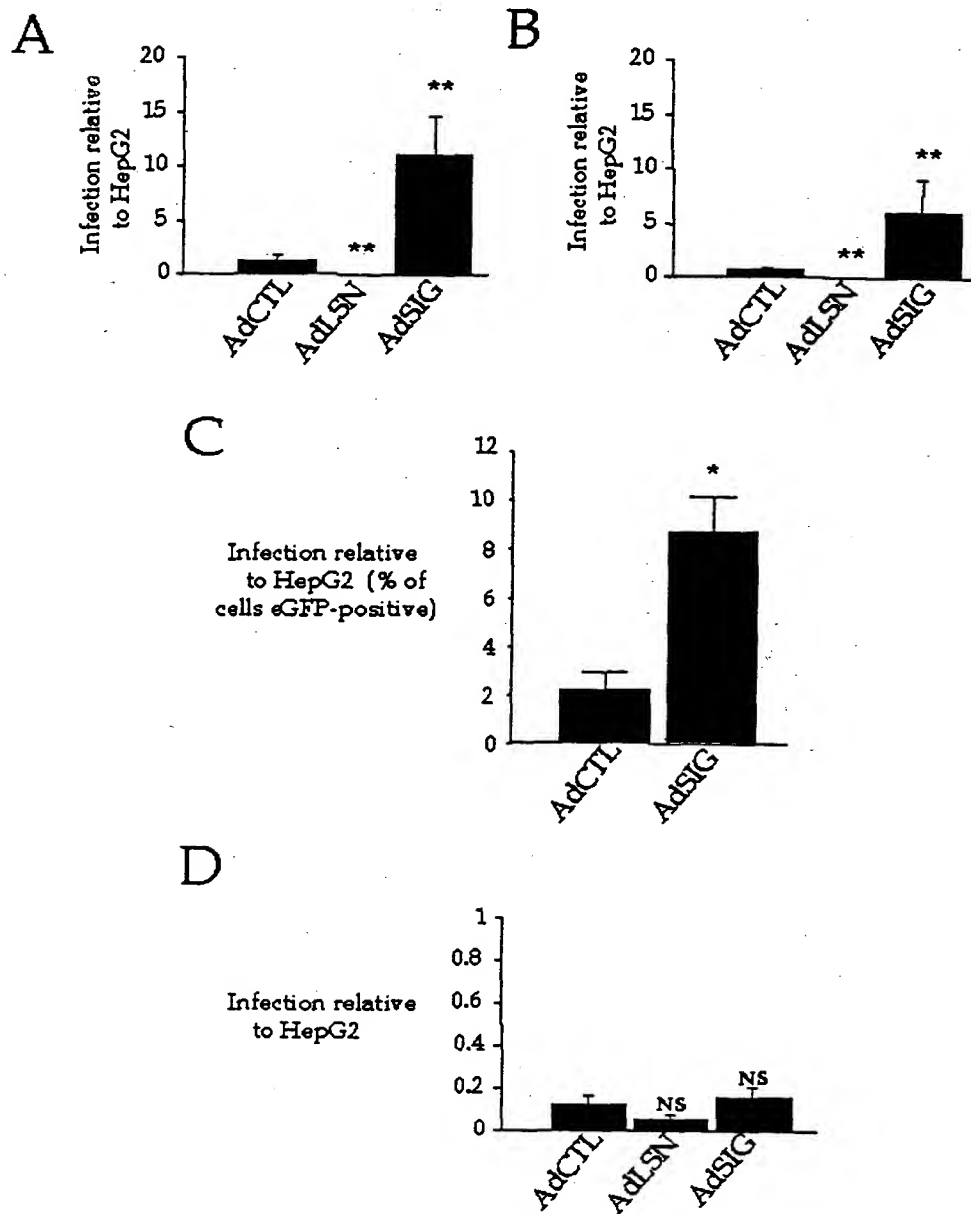
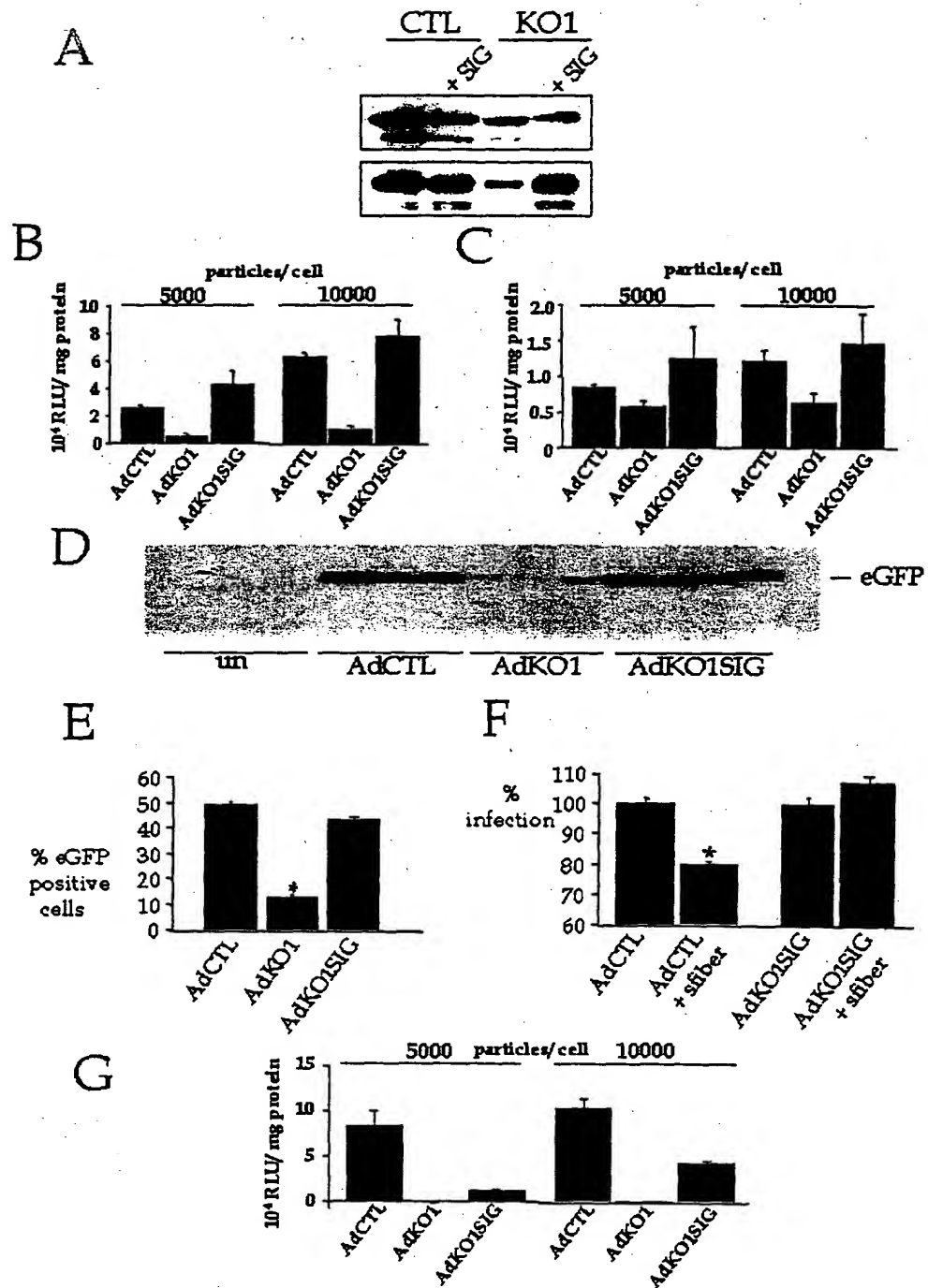
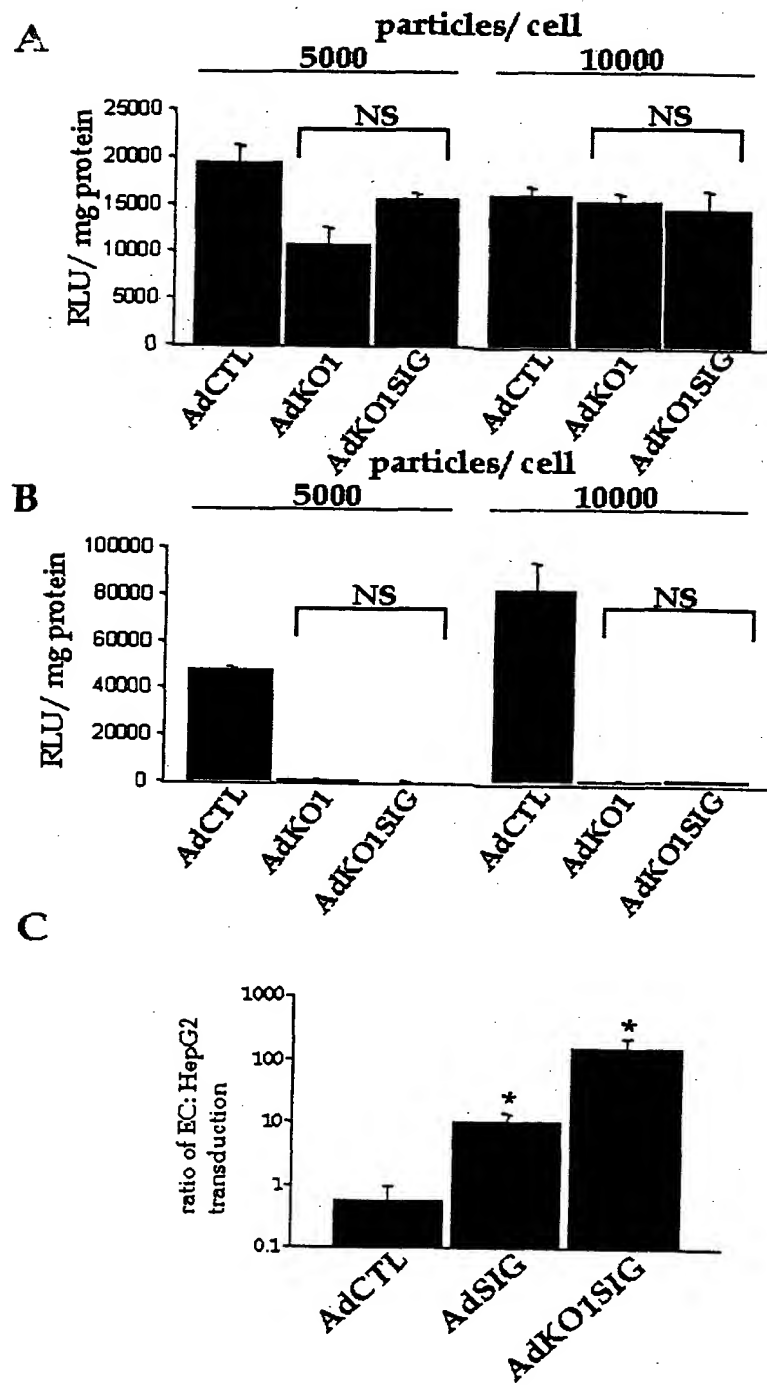
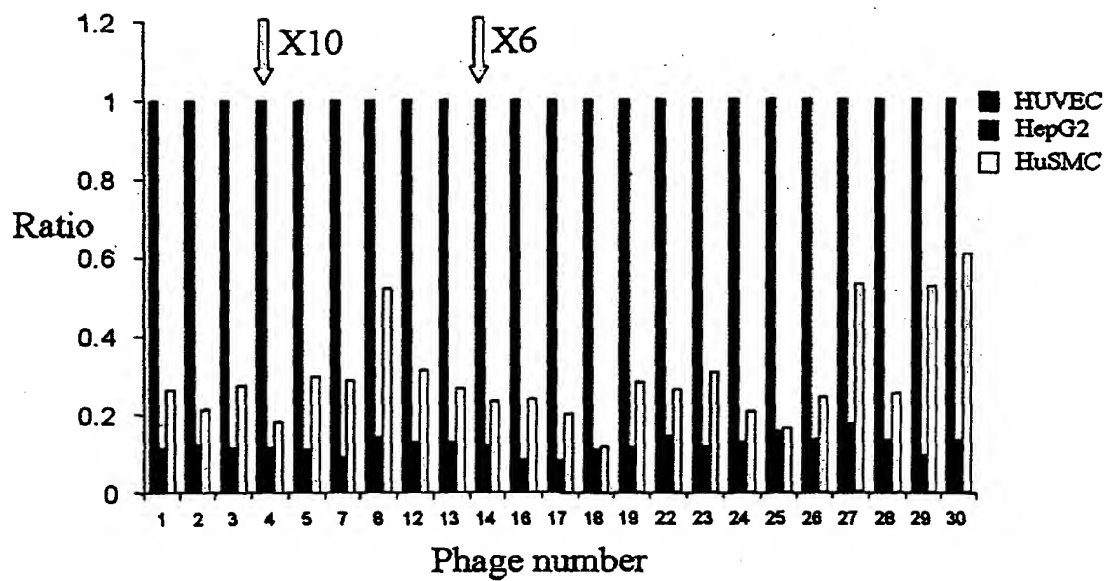
**FIGURE 15**

FIGURE 16

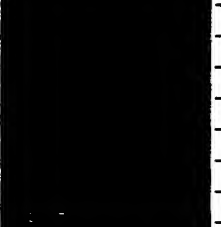


**FIGURE 17**

**FIGURE 18**

## FIGURE 19

1 5	----	MSNNPIRPPTS	G-	12	39 25	----	LSTPLPYDMRR	S-	12
2 10	----	MSNNPIRPPTS	G-	12	40 4	--	MSLTTPPAVARP-	--	12
3 27	----	MSTPPIREQAA	H-	12					
4 22	----	MSQTPYARPOY	V-	12	41 6	--	MSLTTPPAVARP-	--	12
					42 9	--	MSLTTPPAVARP-	--	12
5 53	---	MSSPTVSSAPQY	--	12	43 11	--	MSLTTPPAVARP-	--	12
6 39	---	LQPPSMITHPST	--	12	44 15	--	MSLTTPPAVARP-	--	12
7 43	---	LQPPSMITHPST	--	12					
8 1	--	MAMPQPADHNNS-	--	12	45 33	--	MSLTTPPAVARP-	--	12
					46 34	--	MSLTTPPAVARP-	--	12
9 45	--	MLMPQPAHHNNS-	--	12	47 41	--	MSLTTPPAVARP-	--	12
10 67	--	MGMTVPENLIVQ-	--	12	48 47	--	MSLTTPPAVARP-	--	12
11 68	--	MGMTVPENLIVQ-	--	12					
12 2	--	VSGMSVPVQLAR--	--	12	49 48	--	MSLTTPPAVARP-	--	12
					50 42	----	LTPPNQVLNPL	Y-	12
13 3	---	MTQTPR-TTPWP	D-	12	51 29	---	MTPIATSIPPQM	--	12
14 28	---	MTNLPT-VTQFP	P-	12	52 35	---	MTQQPPLPHPAK	--	12
15 23	---	MTSNPH-LNPGP	R-	12					
16 52	--	SMRGLPE-LNPRI	--	12	53 58	----	MAINDTYPPPRP	--	12
					54 32	----	MTSPHPQTPNL	T-	12
17 63	---	LTSPFSTP--LNPR-	--	12	55 54	---	VLSMQTPPTPLL	--	12
18 70	---	LTSPFSTP--LNPR-	--	12	56 30	--	MTPTTPIPSPLO-	--	12
19 8	---	MTGSQQT LHPPP	--	12					
20 61	---	MQPRPQTLTPAS	--	12	57 24	--	MGHNINIPRTPL-	--	12
					58 60	---	LAQNPIYRAHPH	--	12
21 26	---	MTRIQDSPYDLR	--	12	59 62	----	LTVPVPVSFAV	H-	12
22 69	---	MTPIQSTQYPHS	--	12	60 66	----	ANTPPHTILST	E-	12
23 13	---	MNMTPPPHSPPK	--	12					
24 16	--	AMSMTTMPHSPN-	--	12	61 17	---	MSDLLIEYPPYI	--	12
					62 18	----	MTLPHEL RDGA	L-	12
25 14	-----	MTPFPTSNEA	NL	12	63 36	----	LAKPLPTTSNT	G-	12
26 20	-----	MTPFPTSNEA	NL	12	64 37	----	LSKPIPHIPSS	IG	13
27 31	-----	MTPFPTSNEA	NL	12					
28 40	-----	MTPFPTSNEA	NL	12	65 49	---	SSRIPGFPDPLH	--	12
					66 38	---	CICRGVGCCLLL	--	12
29 51	-----	MTPFPTSNEA	NL	12	67 44	-----	AFPMVGGPDH	FR	12
30 57	-----	MTPFPTSNEA	NL	12	68 46	---	AQAMANPLGSHI	--	12
31 21	-----	NPEPTIDE-	--	8					
32 64	-----	NPEPTIDE-	--	8	69 55	----	THAMSHLDKAH	--	11
					70 50	-----	-----	--	0
33 7	-	MTQVYTPPPTST--	--	12					
34 59	----	MMPPPTSLPS	PS	12					
35 12	---	MATQPLSGSRLS	G-	13					
36 65	---	MAGQPKDSSKTL	--	12					
37 56	---	MAVQPPNTSTSN	--	12					
38 19	----	AAVPPPYVMSR	P-	12					



```

---MAGQPKDSSSKTL---
---MQPRPQTLTPAS---
---MTNLPT-VTQFPP-
---MSSPTVSSAPQY-
---LTPPNQVLNPLY-
---MTPIATSIPPQM---
---MTSPHPQTPNLT-
---VLSMQTPPTPLL---
---MGHNINIPRTPL---
---LAQNPIYRAHPH---
---LTVFPVVSFAVH-
---ANTPPHTILSTE-
---MSDLLIEYPPYI-
---MTLPHELRDGAL-
---SSRIPGFDPDLH-
---CICRGVGCCLLL---
---AFPMVGGPDHFR-
---AQAMANPLGSHI---
---THAMSHLDKAH---

```